

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2005, 01:55:29 ; Search time 1933 Seconds
(without alignments)
10030.407 Million cell updates/sec

Title: US-10-786-065-3_COPY_50000_50409

Perfect score: 410
Sequence: 1 aatcagataatcatcgag.....attatgctgagattcttga 410

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410	100.0	5332	6	AR265351 Sequence
2	410	100.0	5332	6	AX571875 Sequence
3	374.4	91.3	112748	9	AC007242 Homo sapi
4	127.4	31.1	2422	9	AK091710 Homo sapi
5	87.4	21.3	2203	6	AR265350 Sequence
6	87.4	21.3	2203	6	AX571873 Sequence
7	75.8	18.5	161010	2	AC132361 Mus muscu
8	75.8	18.5	173131	10	AC116995 Mus muscu
9	71.4	17.4	179341	2	AC128908 Rattus no
10	71.4	17.4	295449	2	AC105819 Rattus no
11	68	16.6	1828	9	AK131512 Homo sapi
12	67	16.3	888	6	AX803407 Sequence
13	66	16.1	481	6	AR175616 Sequence
14	66	16.1	481	6	AR236733 Sequence
15	66	16.1	1077	6	AX056403 Sequence
16	66	16.1	1308	6	AR265352 Sequence
17	66	16.1	1308	6	AX571876 Sequence
18	66	16.1	1308	6	AX772798 Sequence
19	66	16.1	1376	6	AX644241 Sequence

20	66	16.1	1534	6	AX772791	Sequence
21	66	16.1	1534	6	AX772795	Sequence
22	66	16.1	1534	9	AB053308	Homo sapi
23	66	16.1	1584	6	AX772794	Sequence
24	66	16.1	1628	6	AX772799	Sequence
25	66	16.1	2305	9	BC038807	Homo sapi
26	64.4	15.7	3675	9	BM807539	Homo sapi
27	48.2	11.8	7218	6	I66494	Sequence 14
28	43.2	10.5	204534	2	AC084400	Mus muscu
c 29	43	10.5	82604	9	AL500522	Human DNA
c 30	43	10.5	166387	2	AC145234	Homo sapi
c 31	42.2	10.3	112510	2	AC120200	Danio rer
c 32	42.2	10.3	158694	2	AC144471	Felis cat
c 33	41.6	10.1	153539	2	AL591168	Homo sapi
c 34	41.6	10.1	223196	2	AL290335	Rattus no
c 35	41.6	10.1	286395	2	AC125732	Rattus no
c 36	41.6	10.1	292171	2	AC091244	Rattus no
37	41.6	10.1	326700	2	AC134362	Rattus no
38	41.6	10.1	332668	2	AC130158	Rattus no
c 39	41.6	10.1	333622	2	AC111475	Rattus no
c 40	41.2	10.0	153647	9	AP002979	Homo sapi
41	41.2	10.0	167139	9	AC087710	Homo sapi
c 42	41.2	10.0	168736	2	AC019042	Homo sapi
c 43	41.2	10.0	213751	10	AC124524	Mus muscu
44	41	10.0	75153	2	AC100376	Mus muscu
c 45	41	10.0	146974	10	AC121919	Mus muscu

ALIGNMENTS

RESULT 1	AR265351	Sequence 3 from patent US 6492154.	5332 bp	DNA	linear	PAT 10-APR-2003
LOCUS	AR265351					
DEFINITION	AR265351					
ACCESSION	AR265351					
VERSION	AR265351.1	GI:29693854				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 5332)					
AUTHORS	Yan, C., Ketchum, K.A., Di Francesco, V. and Beasley, E.M.					
TITLE	Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof					
JOURNAL	Patent: US 6492154-A 3 10-DEC-2002;					
FEATURES	Location/Qualifiers					
source	1..5332					
	/organism="unknown"					
	/mol_type="genomic DNA"					

ORIGIN	Query Match	100.0%;	Score 410;	DB 6;	Length 5332;
	Best Local Similarity	100.0%;	Pred. No. 8.2e-114;		
	Matches 410;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AATCATGATTAATCATGAGTAAATGTTCACTGATGAGAACATGACTTTGAGCAAGGCTG	60		
Db	50000	AATCATGATTAATCATGAGTAAATGTTCACTGATGAGAACATGACTTTGAGCAAGGCTG	50059		
Qy	61	TATGATGCTCTGAGAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	120		
Db	50060	TATGATGCTCTGAGAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	50119		
Qy	121	ATTACAGTTTTCCTCCAGAACACCAACGTTTGAACACCTCAAGTTTCTTCTCGTATA	180		
Db	50120	ATTACAGTTTTCCTCCAGAACACCAACGTTTGAACACCTCAAGTTTCTTCTCGTATA	50179		
Qy	181	CATCAGCTGGTGTGATGCAATGGGACATACCATCTGACGCTTCCCTGTTTCCCTGATT	240		
Db	50180	CATCAGCTGGTGTGATGCAATGGGACATACCATCTGACGCTTCCCTGTTTCCCTGATT	50239		
Qy	241	TGTCCTGATGTCCTCCCAATACCTCTTTCCCAACCACTCATCTCCCAACCTCACCTTTCTT	300		

NEIGHBORING SEQUENCE INFORMATION:

REASONING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-53H10, 200 bp overlap; the clone sequenced to the right is RP11-30N8. Actual start of this clone is at base position 100126 of RP11-53H10; actual end is at 112748 of RP11-182H9

The reads used to determine the sequence at the region of base positions 31840 to 112748 consists of numerous polymorphic base changes represented from both NH0182H09 and RP11-309N8. It is unknown which base calls belong to which clone.

FEATURES

Source

[illegible]

Query Match	91.3%;	Score 374.4;	DB 9;	Length 112748;
Best Local Similarity	97.8%;	Pred. No. 5.9e-103;		
Matches 401;	Conservative 0;	Mismatches 6;	Indels 3;	Gaps 2;
Qy	1	AATGCATGATAATCATGTCAGTAAATGTTTCAGTGATGAGAAATGACTTTTGACCAAGGCTG	60	
Db	23575	AATGCATGATAATCATGTCAGTAAATGTTTCAGTGATGAGAAATGACTTTTGACCAAGGCTG	23516	
Qy	61	TATGATCTGCCTCAGAAACAAGTGAGTCAGTAAGAATGCAGGCCCGGACCATAGGAATGT	120	
Db	23515	TATGATCTGCCTCAGAAACAAGTGAGTCAGTAAGAATGCAGGCCCGGACCATAGGAATGT	23456	
Qy	121	ATTACAGTTTTCGCCAAGAAACCAACAAGTTTGGAACACTCAAGTTCTTCTTCGTATA	180	
Db	23455	ATTACAGTTTTCGCCAAGAAACCAACAAGTTTGGAACACTCAAGTTCTTCTTCGTATA	23396	
Qy	181	CATCAGCTGGTGATGCATGGGACATACCACTGACGGTTCCTGTCTTCCCTGATT	240	
Db	23395	CATCAGCTGGTGATGCATGGGACATA-CATCTGAGGCTTCCCTGTCTTCCCTGATT	23337	


```

RESULT 6
AX571873 LOCUS AX571873 2203 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 1 from Patent WO02061060.
ACCESSION AX571873
VERSION AX571873.1 GI:26003999
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Van,C., Ketchum,K., di Francesco,V. and Beasley,B.M.
TITLE Isolated human kinase proteins, nucleic acid molecules encoding
human kinase proteins, and uses thereof
JOURNAL Patent: WO 02061060-A 1 08-AUG-2002;
PE Corporation (NY) (US)
FEATURES
source
1..2203
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 21.3%; Score 87.4; DB 6; Length 2203;
Best Local Similarity 98.9%; Pred. No. 2.1e-15;
Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 322 AGGTCTGGAGTCCCTACAGAGGATACTTGCGGGAGTCTCCAGGTACCTACTACTACA 381
|||||
Db 1061 AGGTCTGGAGTCCCTACAGAGGATACTTGCGGGAGTCTCCAGGTACCTACTACTACA 1120
|||||
QY 382 ATCCAGGTAATATGATCTGAGCTTCTGA 410
|||||
Db 1121 ATCCAGGTAATATGATCTGAGCTTCTGA 1149
|||||

RESULT 7
AC132361 LOCUS AC132361 161010 bp DNA linear HTG 03-SEP-2002
DEFINITION Mus musculus chromosome UNK clone RP24-149E13, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
AC132361
VERSION AC132361.1 GI:22657848
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 161010)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 161010)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0149E13
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319

```

```

Consensus quality: 153781 bases at least Q40
Consensus quality: 154797 bases at least Q30
Consensus quality: 155407 bases at least Q20
Insert size: 179000; agarose-fp
Insert size: 159810; sum-of-contigs
Quality coverage: 10.01 in Q20 bases; agarose-fp
Quality coverage: 10.14 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1984: contig of 1984 bp in length
* 1985 2084: gap of unknown length
* 2085 4163: contig of 2079 bp in length
* 4164 4263: gap of unknown length
* 4264 9331: contig of 5068 bp in length
* 9332 9431: gap of unknown length
* 9432 16764: contig of 7333 bp in length
* 16765 16864: gap of unknown length
* 16865 21118: contig of 4254 bp in length
* 21119 21218: gap of unknown length
* 21219 30095: contig of 8877 bp in length
* 30096 30195: gap of unknown length
* 30196 40537: contig of 10342 bp in length
* 40538 40637: gap of unknown length
* 40638 53634: contig of 12997 bp in length
* 53635 53734: gap of unknown length
* 53735 68578: contig of 14844 bp in length
* 68579 89216: gap of unknown length
* 89217 89316: contig of 20538 bp in length
* 89317 108734: contig of 19418 bp in length
* 108735 108835: gap of unknown length
* 108835 159127: contig of 50293 bp in length
* 159128 159227: gap of unknown length
* 159228 161010: contig of 1783 bp in length.
FEATURES
source
1..161010
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clones="RP24-149E13"
1..1984
/note="assembly_name:Contig10"
2085..4163
/note="assembly_name:Contig11"
4264..9331
/note="assembly_name:Contig12"
9432..16764
/note="assembly_name:Contig14"
16865..21118
/note="assembly_name:Contig13"
21219..30095
/note="assembly_name:Contig15"
30196..40537
/note="assembly_name:Contig16"
40638..53634
/note="assembly_name:Contig17"
53735..68578
/note="assembly_name:Contig18"
68679..89216
/note="assembly_name:Contig19"
89317..108734
/note="assembly_name:Contig20"
108835..159127
/note="assembly_name:Contig21"
159228..161010

```

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```
/note="assembly name:Contig9"
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ORIGIN

	Query Match	Best Local Similarity	Score 75.8%; DB 2; Pred. No. 6.9e-12;	Length 161010;
a	293	86; Conservative	0; Mismatches 17; Indels 0; Gaps 0;	
b	59744			
a	353			
b	59804			

RESULT	8
ACLI16995	Mus musculus BAC clone RP23-3C16 from 1, complete sequence.
LOCUS	173131 bp DNA linear ROD 05-NOV-2003
DEFINITION	
ACLI16995	
ACCESSION	
VERSION	GI:21844700
KEYWORDS	HTG.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Eumetazoa; Cephalochordata; Mammalia; Muridae; Murinae; Mus.

1 (bases 1 to 173131)
Holmes, A., Haglund, K. and Spalding, L.
The sequence of *Mus musculus* BAC clone RP23-3C16
Unpublished (2001)
2 (bases 1 to 173131)
Wilson, R.
Sequencing of *Mus musculus*
Unpublished (2001)
3 (bases 1 to 173131)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (05-APR-2002) Genome Sequencing Center, 4444 Forest Park
Submittal, St. Louis, MO 63108, USA

4	(bases 1 to 173131)	
REFERENCE	McPherson,J.D. and Waterston,R.H.	
AUTHORS	Direct Submission	
TITLE	Submitted (02-MAY-2002) Genome Sequencing Center, 4444 Forest Park	
JOURNAL	Parway, St. Louis, MO 63108, USA	
5	(bases 1 to 173131)	
REFERENCE	McPherson,J.D. and Waterston,R.H.	
AUTHORS	Direct Submission	
TITLE	Submitted (16-JUL-2002) Genome Sequencing Center, 4444 Forest Park	
JOURNAL	Parway, St. Louis, MO 63108, USA	
6	(bases 1 to 173131)	

AUTHORS Wilson, K.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
The submitted version replaced q1:20389753.

```

----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
-----
Genus object name: M RA0003C16

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION: The RPCR-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or used coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
 _____ is the entire insert of the clone.

```

FEATURES
source
1. 173131
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="1"
/map="1"

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repeat_region	1094..1097
	/rpt_family="Alu"
repeat_region	1098..1194
	/rpt_family="B4"
repeat_region	1643..1708
	/rpt_family="TD"
repeat_region	2034..2233
	/rpt_family="B2"
repeat_region	2401..2762
	/rpt_family="MaLR"
repeat_region	3195..3410
	/rpt_family="L2"
repeat_region	3450..3544
	/rpt_family="MaLR"
repeat_region	4140..4860
	/rpt_family="L1"
repeat_region	4937..4991
	/rpt_family="ERV1"
repeat_region	5137..5192
	/rpt_family="L1"
repeat_region	5594..5658
	/rpt_family="ERV1"
repeat_region	6208..6606
	/rpt_family="ERVK"
repeat_region	6754..7097
	/rpt_family="ERVK"
repeat_region	7191..7410
	/rpt_family="L1"
repeat_region	7415..7513
	/rpt_family="L1"
repeat_region	9015..9925
	/rpt_family="B2"
repeat_region	9683..9836
	/rpt_family="B4"
repeat_region	9708..9843
	/rpt_family="Alu"
repeat_region	9876..9990
	/rpt_family="B2"
repeat_region	10126..10319
	/rpt_family="L2"
repeat_region	10456..10637
	/rpt_family="B2"
repeat_region	12237..12855

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Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Direct Submission

Unpublished
2 (bases 1 to 179341)
Worley, K. C.

Direct Submission

Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 179341)

Direct Submission

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23911240. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: KBDA
Center clone name: CH230-320D4
----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 151376 bases at least Q40
Consensus quality: 153458 bases at least Q30
Consensus quality: 155000 bases at least Q20
Estimated insert size: 152913; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 178124: contig of 178124 bp in length
* 178125 178224: gap of unknown length
* 178225 179341: contig of 1117 bp in length.

FEATURES
Location/Qualifiers

1..179341

/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-320D4"
1..2063

misc_feature

2565..3931

misc_feature

5301..5700

misc_feature

complement(176332..177098)

misc_feature

/note="clone_boundary"

clone_end:Sp6
site:
end_sequence:BZ171386"

ORIGIN

Query Match 17.4%; Score 71.4; DB 2; Length 179341;
Best Local Similarity 83.5%; Pred. NO. 1.5e-10;
Matches 81; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 294 CTTCTTTCTTTCTTTGGCTTTATATAGGTGCTGGAGTCCCTACAGAGATCTTGG 353
DB 87089 CCTTGGTCTCTTTCTTGGCTCTGTAGTACTGGAGTCCCTACGAGGACACCTGG 87148
QY 354 CCGGGAGTCTCCAAGCTACCTAACTCAATCAGGTA 390
DB 87149 CTTGGGCTCTCCAAGCTGCTAACTCAATCAGGTA 87185

RESULT 10

AC105819/c

LOCUS

DEFINITION

AC105819.4 GI:23603215

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

Rattus norvegicus

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 295449)

Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anylebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Devila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,

Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogue, M.,

Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorenshewa, L., Louseged, H., Lozada, R. J., Lu, X., Ma, J.,

Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,

Mangum, B., Mapua, P., Martin, K., Martin, R., Martinec, E.,

Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,

Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,

Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwakoemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,

Pasternak, S., Paul, H., Perez, A., Perez, L., Primus, E., Pu, L. L.,

Plopper, F., Poindexter, A., Popovic, D., Primus, E., Reigh, R.,

Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,

Reilly, B., Reilly, T., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,

Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,

Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smajls, D.,

Sneed, A., Sodergren, E., Song, X. Z., Sorelle, R., Sosa, J.,

Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,

RESULT 11
AK131512 1828 bp mRNA linear PRI 07-MAY-2004
LOCUS Homo sapiens cDNA FLJ16732 fis, clone BNGH42005017, moderately
DEFINITION similar to SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (BC 2.7.1.-).
ACCESSION AK131512
VERSION AK131512.1 GI:47077537
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J.,
Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K.,
Yamashita,H., Matsuno,K., Nakamura,Y., Sekine,M., Kikuchi,H.,
Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K.,
Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1828)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 252-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
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CDS
ORIGIN
Query Match 16.6%; Score 68; DB 9; Length 1828;
Best Local Similarity 100.0%; Pred. No. 1.7e-09; Indels 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 0;
QY 322 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAAGCTACCTACTACA 381
Db 967 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAAGCTACCTACTACA 1026
QY 382 ATCCAGGT 389
Db 1027 ATCCAGGT 1034

QY 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
|||||
Db 225 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 284
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QY 382 ATCCAG 387
|||||
Db 285 ATCCAG 290

RESULT 14
AR236733
LOCUS AR236733 481 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 14 from patent US 6465232.
ACCESSION AR236733
VERSION AR236733.1 GI:27280884
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 481)
AUTHORS Robison,K.E.
TITLE Nucleic acid molecules encoding human kinase and phosphatase
homologues and uses therefor
JOURNAL Patent: US 6465232-A 14 15-OCT-2002;
FEATURES Location/Qualifiers
source
1..481
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ORIGIN

Query Match 16.1%; Score 66; DB 6; Length 481;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
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Db 225 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 284
|||||
QY 382 ATCCAG 387
|||||
Db 285 ATCCAG 290

RESULT 15
AX056403
LOCUS AX056403 1077 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 47 from Patent WO0073469.
ACCESSION AX056403
VERSION AX056403.1 GI:12229110
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Plowman,G.D., Martinez,R., Whyte,D. and Sudersanam,S.
TITLE Protein kinases
JOURNAL Patent: WO 0073469-A 47 07-DEC-2000;
Sugen, Inc. (US)
FEATURES Location/Qualifiers
source
1..1077
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 437 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 496
QY 382 ATCCAG 387
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Db 497 ATCCAG 502

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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990a:*
3: Geneseqn2000a:*
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5: Geneseqn2001bs:*
6: Geneseqn2002a:*
7: Geneseqn2002bs:*
8: Geneseqn2003a:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410	100.0	5332	6	AAL48890 Human pft
2	87.4	21.3	2203	6	AAL48889 Human pft
3	68	16.6	1828	12	ADM16422 DNA encod
4	67	16.3	888	10	ABZ77160 Human pro
5	66	16.1	481	6	AAS17061 Human pro
6	66	16.1	481	10	AAD61613 Human pro
7	66	16.1	481	10	ABX14985 Human pro
8	66	16.1	1077	4	AAF44668 Human pft
9	66	16.1	1077	12	ADI29366 Human MAR
10	66	16.1	1308	6	AAL48891 Human pft
11	66	16.1	1308	9	ACC79970 Human ser
12	66	16.1	1311	10	ADC30755 Human nov
13	66	16.1	1376	8	ABA00722 Human KPF
14	66	16.1	1534	9	ACC79969 Human ser
15	66	16.1	1534	9	ACC79967 Human ser
16	66	16.1	1584	9	ACC79968 Human ser
17	66	16.1	1628	9	ACC79971 Human ser
18	66	16.1	2140	11	ADL22554 Human dis
19	66	16.1	2250	12	ADJ96563 Human cyc
20	40.4	9.9	189013	8	ACF62741 Cancer ba
21	40.4	9.9	189013	8	Adb20856 MRP1 base

ALIGNMENTS

RESULT 1

AAL48890

ID AAL48890 standard; DNA; 53332 BP.

XX AC AAL48890;

XX DT 24-OCT-2002 (first entry)

XX DE Human pftaire family kinase gene.

XX KW Human; pftaire family kinase; kinase; enzyme; testis; brain; cytosolic;

XX KW uterus endometrium adenocarcinoma; lung fibroblast; splice form;

XX KW kidney renal cell adenocarcinoma; gene therapy; gene; ds.

XX OS Homo sapiens.

XX FH Key

XX FT variation

XX FT variation

XX FT variation

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

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XX FT CDS

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AC AAL4889;
 XX 24-OCT-2002 (first entry)
 DT
 XX Human Pftaire family kinase splice form 1 coding sequence.
 DE
 XX Human; Pftaire family kinase; kinase; enzyme; testis; brain; cytosolic;
 KW uterus endometrium adenocarcinoma; lung fibroblast; splice form;
 KW kidney renal cell adenocarcinoma; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 5'UTR 1..117
 FT /*tag= a
 FT CDS 118..1149
 FT /*tag= b
 FT /*product= "kinase"
 FT 3'UTR 1149..2203
 FT /*tag= c
 XX
 PN WO200261060-A2.
 XX
 XX 08-AUG-2002.
 PD
 XX 17-JAN-2002; 2002WO-US001106.
 PF
 XX 31-JAN-2001; 2001US-0265151P.
 PR 09-MAR-2001; 2001US-00801861.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Yan C, Ketchum K, Di Francesco V, Beasley EM;
 PI WPI; 2002-608515/65.
 DR P-PSDB; AAO18613.
 XX
 XX New human kinase peptide and nucleic acid molecule, useful for treating
 PT disorders associated with abnormal expression of kinase protein, e.g.
 PT adenocarcinoma of uterus or lung, in drug screening assays and
 PT pharmacogenomic analysis.
 XX
 XX Claim 4; Fig 1; 131pp; English.
 PS
 XX The present invention provides the protein, cDNA and gene sequences of
 CC two splice variants of a human Pftaire family kinase. The sequences are
 CC specifically expressed in the human testis, brain, uterus endometrium
 CC adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinomas, and
 CC can be used to treat related diseases. The present sequence is the cDNA
 CC of splice variant 1 of the invention
 XX
 XX Sequence 2203 BP; 657 A; 460 C; 538 G; 548 T; 0 U; 0 Other;
 SQ
 Query Match 21.3%; Score 87.4; DB 6; Length 2203;
 Best Local Similarity 98.9%; Pred. No. 1.3e-17;
 Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 322 AGGTCTGGAGTCCCTACAGAGGATCTTGCCGGGAGTCTCCAGGCTACTACTACTACA 381
 DB 1061 AGGTCTGGAGTCCCTACAGAGGATCTTGCCGGGAGTCTCCAGGCTACTACTACTACA 1120
 QY 382 ATCCAGGTAATATTGATCTGAGCTTCTGA 410
 DB 1121 ATCCAGGTAATATTGATCTGAGCTTCTGA 1149
 RESULT 3
 ADM16422
 ID ADM16422 standard; DNA; 1828 BP.
 XX
 AC ADM16422;
 XX
 DT 17-JUN-2004 (first entry)

XX DNA encoding human kinase protein, seq id 1.
 DE
 XX Cytostatic; cardiant; neuroprotective; nootropic; antiinfertility;
 KW vulnerable; antidiabetic; kinase; cancer; heart disease;
 KW Alzheimer's disease; infertility; wound; diabetes; neurological disease;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 87..1124
 FT /*tag= a
 FT /*product= "kinase"
 XX
 PN WO2004024913-A1.
 XX
 XX 25-MAR-2004.
 PD
 XX 10-SEP-2003; 2003WO-JP011552.
 PF
 XX 10-SEP-2002; 2002JP-00264345.
 PR
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA (ZOE-) ZOEGENE CORP.
 XX
 XX Kondo J, Kawai K, Miyama N, Nakajima M, Isogai T, Sugiyama T;
 PI Wakamatsu A, Irie R, Ishii S;
 XX WPI; 2004-270042/25.
 DR P-PSDB; ADM16427.
 XX
 XX Proteins of human origin having kinase activity, useful for prevention
 PT and treatment of kinase-associated diseases including cancer, heart
 PT disease and Alzheimer's disease.
 XX
 XX Claim 4; SEQ ID NO 1; 105pp; Japanese.
 PS
 XX The invention relates to four proteins of human origin (I) having kinase
 CC activity, and to proteins derived from these by addition, deletion and/or
 CC substitution of one or more amino acid residues, and having similar
 CC activity. The proteins and other aspects of the invention are useful for
 CC the prevention and treatment of kinase-associated diseases including
 CC cancer, heart disease, Alzheimer's disease, infertility, wounds, diabetes
 CC and neurological diseases. The current sequence represents a human DNA
 CC encoding a protein having kinase activity.
 XX
 XX Sequence 1828 BP; 496 A; 398 C; 450 G; 484 T; 0 U; 0 Other;
 SQ
 Query Match 16.6%; Score 68; DB 12; Length 1828;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 322 AGGTCTGGAGTCCCTACAGAGGATCTTGCCGGGAGTCTCCAGGCTACTACTACA 381
 DB 967 AGGTCTGGAGTCCCTACAGAGGATCTTGCCGGGAGTCTCCAGGCTACTACTACA 1026
 QY 382 ATCCAGGT 389
 DB 1027 ATCCAGGT 1034
 RESULT 4
 ABZ77160
 ID ABZ77160 standard; cDNA; 888 BP.
 XX
 AC ABZ77160;
 XX
 DT 07-MAY-2003 (first entry)
 XX
 DE Human protein kinase encoding cDNA SEQ ID NO:69.
 XX
 KW Human; protein kinase; enzyme; antiaesthmic; antiinflammatory;

Thu Jan 13 09:56:04 2005

antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatic; immunosuppressive; vulnery; gene therapy; COPD; asthma; migraine; chronic obstructive pulmonary disease; non-insulin dependent diabetes; Parkinson's disease; myocardial infarction; inflammatory bowel disease; autoimmune disorder; allograft rejection; graft versus host disease; cancer; leukaemia; wound granulation; gene; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 1..888
/tag= a
/partial
/product= "protein kinase"
/note= "no start or stop codons given"

WO2003000901-A2.
03-JAN-2003.
24-JUN-2002; 2002WO-IB002358.
26-JUN-2001; 2001US-0301098P.
06-NOV-2001; 2001US-032870P.
(DECO-) DECODE GENETICS EHF.
Martinez RAM, Sigurdson GT;
WPI; 2003-201429/19.
P-PSDB; ABP96082.
New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy for treating e.g. Parkinson's disease, migraine, myocardial infarction, allograft rejection or cancers.
Claim 1; Page 85; 258pp; English.
AB277126 to AB277165 encode the human protein kinases given in ABP96048 to ABP96087. The protein kinases have antiasthmatic, antiinflammatory, antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic, immunosuppressive and vulnery activities, and can be used in gene therapy. A protein kinase therapeutic agent from the present invention, particularly a protein kinase gene agonist or antagonist, can be used for treating a disease or condition associated with a protein kinase in an individual. These diseases include chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease, migraine, myocardial infarction, inflammatory bowel disease, autoimmune disorders (e.g. allograft rejection or graft vs. host disease), cancers (e.g. leukaemias) or wound granulation

Sequence 888 BP; 214 A; 234 C; 207 G; 233 T; 0 U; 0 Other;
Query Match 16.3%; Score 67; DB 10; Length 888;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAGTACTCTACTACTACA 381
647 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAGTACTCTACTACTACA 706
382 ATCCAGG 388
707 ATCCAGG 713

RESULT 5
AAS17061
ID AAS17061 standard; cDNA; 481 BP.
XX
AC AAS17061;
XX

14-FEB-2002 (first entry)
Human protein kinase cDNA mine42958human_c1.
Human; ss; protein kinase; mine42958human_c1; cytostatic; antianginal; hypotensive; cardiant; cardiovascular disorder; heart failure; hypertension; atrial fibrillation; dilated cardiomyopathy; cancer; idiopathic cardiomyopathy; angina; proliferative disorder; cancer; melanoma; prostate cancer; cervical cancer; breast cancer; colon sarcoma; gene therapy.

Homo sapiens.
US6309849-B1.
30-OCT-2001.
31-AUG-1999; 99US-00387212.
31-AUG-1999; 99US-00387212.
(MILL-) MILLENNIUM PHARM INC.
Robison KE;
WPI; 2002-048371/06.
Identifying compound which binds to a Kinase, useful for treating diseases e.g. cancer, by contacting kinase with test compound and detecting its binding to the kinase.

Example 1; Fig 14; 45pp; English.

The invention relates to identifying a compound which binds to a Kinase (encoded by a nucleotide sequence of 1868, 403, 545, 361, 473, 3001, 526, 683 or 1448 base pair (bp) as given in the specification) comprising for contacting the kinase with a test compound under suitable conditions for binding, and detecting binding of the compound to the kinase. The method is useful for identifying a compound which binds to the kinase and also for isolating compounds which modify the activity of the kinase. The identified compounds are useful for treating a subject having a disorder characterised by aberrant kinase activity where the disorder includes cellular growth related disorders which includes a disorder, disease, or condition characterised by a deregulation, e.g. an upregulation or a downregulation, of cellular growth. Cellular growth deregulation due to deregulation of cellular proliferation, cell cycle progression, cellular differentiation and/or cellular hypertrophy, cardiovascular disorders such as heart failure, hypertension, atrial fibrillation, dilated cardiomyopathy, idiopathic cardiomyopathy, or anginal, proliferative disorders such as cancer (including melanoma, prostate cancer, cervical, breast, colon sarcoma). The kinases and antibodies raised against them are useful in one or more method such as screening assays, predictive medicine and methods of treatment. The nucleic acid molecules are useful for expressing kinase and phosphatase protein (e.g. in gene therapy applications), to detect kinase and phosphatase mRNA or a genetic alteration in a kinase and phosphatase gene and to modulate kinase and phosphatase activity. The present sequence is a cDNA for a human protein kinase

Sequence 481 BP; 100 A; 136 C; 123 G; 122 T; 0 U; 0 Other;
Query Match 16.1%; Score 66; DB 6; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAGTACTCTACTACTACA 381
225 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAGTACTCTACTACTACA 284
382 ATCCAG 387
285 ATCCAG 290

```
RESULT 6
AAD61613
ID AAD61613 standard; cDNA; 481 BP.
XX
AC AAD61613;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human protein kinase cDNA, 42958S1.
XX
KW Kinase; phosphatase; drug target; therapy; gene; human; ss.
XX
OS Homo sapiens.
XX
XX US2003104505-A1.
XX
PD 05-JUN-2003.
XX
PF 12-APR-2002; 2002US-00121925.
XX
PR 31-AUG-1999; 99US-00387212.
XX
PR 07-SEP-2001; 2001US-00948802.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Robison KE;
XX
DR WPI; 2003-801234/75.
XX
XX Detecting and modulating the activity of specified kinases and
PT phosphatases which are potentially useful as drug targets.
XX
PS Claim 1; Fig 14; Opp; English.
XX
XX The present invention relates to a method for detecting the presence of a
CC kinases or phosphatases encoded by nucleotides. The kinases and
CC phosphatases and their encoding nucleic acids are potentially useful as
CC drug targets. The present invention may also be useful in diagnosing
CC disease. The present sequence is human protein kinase cDNA
XX
XX Sequence 481 BP; 100 A; 136 C; 123 G; 122 T; 0 U; 0 Other;
SQ
Query Match 16.1%; Score 66; DB 10; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 322 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACTCACTACTACA 381
DB 225 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACTCACTACTACA 284
QY 382 ATCCAG 387
DB 285 ATCCAG 290
XX
RESULT 7
ABX14985
ID ABX14985 standard; cDNA; 481 BP.
XX
AC ABX14985;
XX
XX 13-MAR-2003 (first entry)
XX
XX Human protein kinase cDNA mine42958human_s1.
XX
XX Human; ss; protein kinase; mine42958human_s1; cancer; cytostatic;
KW antiangiinal; hypotensive; cardiant. proliferative disorder;
KW cellular growth related disorder; cardiovascular disorder; heart failure;
KW hypertension; atrial fibrillation; dilated cardiomyopathy;
KW idopathic cardiomyopathy; angina.
XX
XX Homo sapiens.
OS
```

```
XX US6465232-B1.
XX
XX 15-OCT-2002.
XX
XX 07-SEP-2001; 2001US-00948802.
XX
XX 31-AUG-1999; 99US-00387212.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Robison KE;
XX
XX WPI; 2003-147067/14.
XX
XX Novel human kinase and phosphatase nucleic acid molecules useful for
PT treating cellular proliferative disorders such as cancer, cardiovascular
PT diseases, hypertension, heart failure and angina.
XX
XX Example 1; Fig 14; 47pp; English.
XX
XX The invention relates to an isolated human kinase and phosphatase nucleic
CC acid molecule appearing as ABX14972, ABX14973, ABX14975, ABX14976, and
CC ABX14978-ABX14981, or their complement. Also included are: (1) an
CC isolated nucleic acid molecule which is at least 90 % identical to the
CC nucleotide sequence ABX14973 or ABX14975, or 95 % identical to the
CC complement, where the nucleic acid molecule encodes a polypeptide having
CC a kinase activity; (2) An isolated nucleic acid molecule which hybridizes
CC to ABX14973, ABX14975, ABX14976, and ABX14978 in 6X saline sodium citrate
CC (SSC) at 45 plusOC, followed by one or more washes in 0.2X SSC, 0.1%
CC sodium dodecyl sulphate (SDS) at 65 plusOC, where the molecule encodes a
CC polynucleotide, operatively linked to a recombinant regulatory sequence;
CC and (4) expressing a polypeptide by culturing a host cell comprising the
CC vector under conditions in which the nucleic acid molecule is expressed.
CC The nucleic acids are useful as modulating agents in regulating a variety
CC of cellular processes, and fragments are useful as primers or
CC hybridisation probes for detecting kinase and phosphatase encoding
CC nucleic acids. The nucleic acids are useful for treating proliferative
CC disorders such as cancer and cellular growth related disorders including
CC cardiovascular disorders such as heart failure, hypertension, atrial
CC fibrillation, dilated cardiomyopathy, idiopathic cardiomyopathy or
CC angina. The present sequence is one of the human kinase or phosphatase
CC cDNAs of the invention
XX
XX Sequence 481 BP; 100 A; 136 C; 123 G; 122 T; 0 U; 0 Other;
SQ
Query Match 16.1%; Score 66; DB 10; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 322 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACTCACTACTACA 381
DB 225 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACTCACTACTACA 284
QY 382 ATCCAG 387
DB 285 ATCCAG 290
XX
RESULT 8
AAF44668
ID AAF44668 standard; cDNA; 1077 BP.
XX
XX AAF44668;
XX
XX 27-MAR-2001 (first entry)
XX
XX Novel protein kinase cDNA, SEQ ID NO: 48.
XX
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW
```

US-10-786-065-3_copy_50000_50409.rng

Thu Jan 13 09:56:04 2005

Alzheimer's disease; neurodegenerative disorder; hyperproliferative disorder; cytostatic.

Homo sapiens.
US2003232771-A1.

18-DEC-2003.

17-JUN-2002; 2002US-00174319.

17-JUN-2002; 2002US-00174319.

(ISIS-) ISIS PHARM INC.

Ward DT, Freier SM, Dobie KW;

WPI; 2004-052188/05.

P-PSDB; ADI29248.

New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3); useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.

Disclosure; Fig 2; 233pp; English.

The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3); that specifically hybridizes with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated cDNA included in the figures but not mentioned anywhere else in the specification.

Sequence 1077 BP; 269 A; 257 C; 248 G; 303 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 12; Length 1077;

Best Local Similarity 100.0%; Pred. No. 9.6e-11; Indels 0; Gaps 0; Matches 66; Conservative 0; Mismatches 0;

322 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACTACTACA 381
|||||
437 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACTACTACA 496

382 ATCCAG 387

497 ATCCAG 502

RESULT 10

ADL48891

ID AAL48891 standard; cDNA; 1308 BP.

XX AAL48891;

XX 24-OCT-2002 (first entry)

Human Pftaire family kinase splice form 2 coding sequence.

Human; Pftaire family kinase; kinase; enzyme; testis; brain; cytostatic; uterus endometrium adenocarcinoma; lung fibroblast; splice form; kidney renal cell adenocarcinoma; gene therapy; gene; ss.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

Homo sapiens.

WO200073469-A2.

07-DEC-2000.

26-MAY-2000; 2000WO-US014842.

28-MAY-1999; 99US-0136503P.

(SUGB-) SUGEN INC.

Plowman GD, Martinez R, Whyte D, Sudersanam S;

WPI; 2001-032161/04.

P-PSDB; AAB65641.

Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.

Example 1; Fig 2; 310pp; English.

The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.

Sequence 1077 BP; 269 A; 257 C; 248 G; 303 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 4; Length 1077;

Best Local Similarity 100.0%; Pred. No. 9.6e-11; Indels 0; Gaps 0; Matches 66; Conservative 0; Mismatches 0;

322 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACTACTACA 381
|||||
437 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACTACTACA 496

382 ATCCAG 387

497 ATCCAG 502

RESULT 9

ADL29366

ID ADL29366 standard; cDNA; 1077 BP.

XX ADL29366;

XX 22-APR-2004 (first entry)

Human MARK3-associated cDNA #36.

Human; ss; antisense gene therapy; MARK3; MAP/microtubule affinity-regulating kinase 3; cancer;

```

FT CDS 1..1306
FT /*tag= a
FT /product= "kinase"
XX WO200261060-A2.
XX 08-AUG-2002.
XX
XX PF 17-JAN-2002; 2002WO-US001106.
XX
XX PR 31-JAN-2001; 2001US-0265151P.
XX 09-MAR-2001; 2001US-00801861.
XX
XX PA (PEKE ) PE CORP NY.
XX
XX PI Yan C, Ketchum K, Di Francesco V, Beasley EM;
XX WPI; 2002-608515/65.
XX P-PSDB; AA018614.
XX
XX New human kinase peptide and nucleic acid molecule, useful for treating
XX PT disorders associated with abnormal expression of kinase protein, e.g.
XX PT adenocarcinoma of uterus or lung, in drug screening assays and
XX PT pharmacogenomic analysis.
XX
XX PS Claim 4; Fig 1; 131pp; English.
XX
XX CC The present invention provides the protein, cDNA and gene sequences of
XX CC two splice variants of a human pftaire family kinase. The sequences are
XX CC specifically expressed in the human testis, brain, uterus endometrium
XX CC adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinomas, and
XX CC can be used to treat related diseases. The present sequence is the cDNA
XX CC of splice variant 2 of the invention
XX
XX SQ Sequence 1308 BP; 328 A; 332 C; 330 G; 318 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 6; Length 1308;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTGCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGTACCTAACTACA 381
Db |||||
944 AGGTGCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGTACCTAACTACA 1003

QY 382 ATCCAG 387
Db |||||
1004 ATCCAG 1009

RESULT 11
ACC79970
ID ACC79970 standard; cDNA; 1308 BP.
XX
XX AC ACC79970;
XX
XX 09-SEP-2003 (first entry)
XX
XX DE Human serine/threonine protein kinase encoding cDNA SEQ ID NO:8.
XX
XX KW Human; serine/threonine protein kinase; kinase; enzyme; cytotostatic;
XX KW antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic;
XX KW cerebroprotective; antiinflammatory; gastrointestinal; hepatotropic;
XX KW gynaecological; uropathic; dermatological; gene therapy; cancer;
XX KW diabetes; central nervous system disorder; CNS disorder; liver disease;
XX KW respiratory disorder; chronic obstructive pulmonary disease; stroke;
XX KW cardiovascular disorder; dermatological disorder; urological disorder;
XX KW gastrointestinal disease; haematological disorder; Alzheimer's disease;
XX KW musculoskeletal disorder; reproductive disorder; Parkinson's disease;
XX KW neuropathic pain; gene; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
```

```

FT CDS 1..1308
FT /*tag= a
FT /product= "serine/threonine protein kinase"
XX WO2003046167-A1.
XX
XX PD 05-JUN-2003.
XX
XX PF 26-NOV-2002; 2002WO-EP013268.
XX
XX PR 27-NOV-2001; 2001US-0333131P.
XX (FARB ) BAYER AG.
XX
XX PI Koehler RH;
XX
XX DR WPI; 2003-505196/47.
XX P-PSDB; ABR57361.
XX
XX New polynucleotide encoding a serine/threonine protein kinase
XX PT polypeptide, useful for diagnosing, preventing or treating diseases
XX PT associated with serine/threonine protein kinase dysfunction, e.g. cancer
XX PT or diabetes.
XX
XX PS Disclosure; Fig 8; 196pp; English.
XX
XX CC The present sequence encodes a human serine/threonine protein kinase (I).
XX CC (I) has cytostatic, antidiabetic, neuroprotective, antiparkinsonian,
XX CC nootropic, cerebroprotective, analgesic, antiinflammatory, hepatotropic,
XX CC gastrointestinal, gynaecological, uropathic and dermatological
XX CC activities, and can be used in gene therapy. Serine/threonine protein
XX CC kinase polynucleotide and polypeptide sequences can be used in
XX CC diagnosing, preventing, ameliorating or treating diseases associated with
XX CC serine/threonine protein kinase dysfunction. They may also be used to
XX CC identify test compounds that may act, for example, as activators or
XX CC inhibitors at the enzyme's active site. The human serine/threonine
XX CC protein kinase and its fragments are also useful in raising specific
XX CC antibodies that can block the enzyme and effectively reduce its activity.
XX CC Human serine/threonine protein kinase sequences can be used in the
XX CC preparation of a medicament for modulating the activity of a serine/
XX CC threonine protein kinase in a disease, e.g. cancer, diabetes, a central
XX CC nervous system (CNS) disorder, a respiratory disorder (including chronic
XX CC obstructive pulmonary disease), a cardiovascular disorder, a
XX CC dermatological disorder, a gastrointestinal or liver disease, a
XX CC haematological disorder, a musculoskeletal disorder, a reproductive
XX CC disorder, or a urological disorder. CNS disorders may include Alzheimer's
XX CC disease, Parkinson's disease, stroke or neuropathic pain
XX
XX SQ Sequence 1308 BP; 328 A; 332 C; 330 G; 318 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 9; Length 1308;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTGCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGTACCTAACTACA 381
Db |||||
944 AGGTGCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGTACCTAACTACA 1003

QY 382 ATCCAG 387
Db |||||
1004 ATCCAG 1009

RESULT 12
ADC30755
ID ADC30755 standard; cDNA; 1311 BP.
XX
XX AC ADC30755;
XX
XX 18-DEC-2003 (first entry)
XX
XX DE Human novel cDNA sequence, SEQ ID NO:837.
XX
XX FH Key Location/Qualifiers
```

KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antitumor; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; gene; ss.
XX Homo sapiens.
XX WO2003029271-A2.
XX 10-APR-2003.
XX 24-SEP-2002; 2002WO-US030474.
XX 24-SEP-2001; 2001US-0324631P.
XX (HYSE-) HYSEQ INC.
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX WPI; 2003-371981/35.
DR P-PSDB; ADC31726.
XX New polynucleotide and polypeptide useful for diagnosing, preventing or
XX treating conditions such as neurodegenerative diseases, anemias, platelet
XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
XX cancer.
XX Claim 1; SEQ ID NO 837; 1185pp; English.
XX The invention relates to 971 novel human cDNA sequences (ADC29919-
XX ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
XX invention also relates to nucleic acid sequences over 99% identical with
XX the novel human cDNAs. The invention additionally encompasses expression
XX vectors and host cells comprising a nucleic acid of the invention; the
XX recombinant production of a polypeptide of the invention; an antibody
XX against a polypeptide of the invention; a method of detecting
XX polynucleotides or polypeptides of the invention; and methods of
XX identifying a compound which binds to a polypeptide of the invention. The
XX invention further discloses methods of preventing, treating or
XX ameliorating a medical condition; kits comprising polynucleotide probes
XX and/or monoclonal antibodies for carrying out the methods of the
XX invention; methods for the identification of compounds that modulate the
XX expression or activity of the polynucleotide and/or polypeptide; and 767
XX contig sequences corresponding to the cDNA sequences of the invention
XX (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
XX -ADC33394). The nucleic acids and polypeptides of the invention, in the
XX useful in diagnostics, drug screening, forensics, gene mapping, in the
XX identification of mutations responsible for genetic disorders or other
XX traits, for assessing biodiversity, and in producing many other types of
XX data and products dependent on DNA and amino acid sequences. They are
XX also used for treating diseases such as Parkinson's disease, Alzheimer's
XX disease and other neurodegenerative diseases, anaemia, platelet
XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
XX cancer. The nucleic acids may also be used as hybridisation probes or
XX primers, and in the recombinant production of a protein. The polypeptides
XX are also useful in generating antibodies, as molecular weight markers,
XX and as food supplements. The present sequence represents a specifically
XX claimed human cDNA sequence of the invention. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1311 BP; 332 A; 328 C; 329 G; 322 T; 0 U; 0 Other;
XX Query Match 16.1%; Score 66; DB 10; Length 1311;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-10;
XX Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGTGCTGGAGTCCCTACAGAGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 893 AGGTGCTGGGAGTCCCTACAGAGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 952
QY 382 ATCCAG 387
DB 953 ATCCAG 958
RESULT 13
ABAO0722
ID ABA00722 standard; cDNA; 1376 BP.
XX ABA00722;
XX 04-MAR-2003 (first entry)
XX Human KPP-7 cDNA, Incyte ID No. 7494145CB1.
XX Gene; kinase; phosphatase; KPP; cell proliferation; arteriosclerosis;
XX atherosclerosis; cirrhosis; hepatitis; polycythemia vera; psoriasis;
XX paroxysmal nocturnal haemoglobinuria; cancer; development; renal tubular acidosis;
XX primary thrombocytopenia; cancer; neurological disorder; Alzheimer's disease;
XX anaemia; mental retardation; Sjogren's syndrome; uveitis; asthma;
XX Parkinson's disease; epilepsy; contact dermatitis; Crohn's disease; allergy;
XX menstrual cycle; autoimmune; inflammation; rheumatoid arthritis; AIDS;
XX autoimmune thyroiditis; glomerulonephritis; Goodpasture's syndrome; gout;
XX diabetes mellitus; Hashimoto's thyroiditis; irritable bowel syndrome;
XX Graves' disease; osteoarthritis; osteoporosis; pancreatitis;
XX multiple sclerosis; mouse; PPTARE kinase; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 298..1263
XX /*tag= a "KPP-7"
XX WO200290530-A2.
XX 14-NOV-2002.
XX 16-JAN-2002; 2002WO-US001369.
XX 18-JAN-2001; 2001US-0263083P.
XX 23-FEB-2001; 2001US-0271117P.
XX 23-FEB-2001; 2001US-0271205P.
XX 16-MAR-2001; 2001US-0276859P.
XX 23-MAR-2001; 2001US-0278504P.
XX 23-MAR-2001; 2001US-0278522P.
XX 29-MAR-2001; 2001US-0280266P.
XX 29-MAR-2001; 2001US-0280510P.
XX (INCY-) INCYTE GENOMICS INC.
XX Lee EA, Walia NK, Baughn MR, Ison CH, Gururajan R, Arvizu C;
PI Yao MG, Jackson JL, Tang TY, Yue H, Tran B, Ding L, Lu DAM;
PI Lal PG, Warren BA;
XX WPI; 2003-111972/10.
DR P-PSDB; AAG79729.
XX New human kinases and phosphatases and polynucleotides, useful for
XX diagnosing, treating or preventing autoimmune or inflammatory disorders
XX (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
XX cancer or hepatitis.
XX Claim 5; Page 144; 144pp; English.
XX The sequences given in ABA00716-23 encode human kinases and phosphatases
XX (KPP). The KPP polypeptides, polynucleotides, and agonists and

antagonists to them, are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with KPP. The protein encoded by this sequence is homologous to mouse PPTAIRE kinase

Sequence 1376 BP; 374 A; 321 C; 342 G; 339 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 8; Length 1376;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAGCTACTACTACA 381
|||||
1088 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAGCTACTACTACA 1147
|||||

382 ATCCAG 387

1148 ATCCAG 1153

RESULT 14

ACCT79969
ID ACC79969 standard; cDNA; 1534 BP.

ACCT79969;

09-SEP-2003 (first entry)

Human serine/threonine protein kinase nucleotide sequence SEQ ID NO:5.

Human; serine/threonine protein kinase; kinase; enzyme; cytostatic; antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic; cerebroprotective; antiinflammatory; gastrointestinal; hepatotropic; gynaecological; uropathic; dermatological; gene therapy; cancer; diabetes; central nervous system disorder; CNS disorder; liver disease; respiratory disorder; chronic obstructive pulmonary disease; stroke; cardiovascular disorder; dermatological disorder; urological disorder; gastrointestinal disease; haematological disorder; Alzheimer's disease; musculoskeletal disorder; reproductive disorder; Parkinson's disease; neuropathic pain; gene; ss.

Homo sapiens.

WO2003046167-A1.

05-JUN-2003.

26-NOV-2002; 2002WO-EP013268.

27-NOV-2001; 2001US-0333131P.

(FARB) BAYER AG.

Koehler RH;

WPI; 2003-505196/47.

New polynucleotide encoding a serine/threonine protein kinase

PT polypeptide, useful for diagnosing, preventing or treating diseases associated with serine/threonine protein kinase dysfunction, e.g. cancer or diabetes.

Disclosure; Fig 5; 196pp; English.

The present sequence represents a human serine/threonine protein kinase (I) related nucleotide sequence from the present invention. (i) has cytostatic, antidiabetic, neuroprotective, antiparkinsonian, nootropic, cerebroprotective, analgesic, antiinflammatory, hepatotropic, gastrointestinal, gynaecological, uropathic and dermatological activities, and can be used in gene therapy. Serine/threonine protein kinase polynucleotide and polypeptide sequences can be used in diagnosing, preventing, ameliorating or treating diseases associated with serine/threonine protein kinase dysfunction. They may also be used to identify test compounds that may act, for example, as activators or inhibitors at the enzyme's active site. The human serine/threonine protein kinase and its fragments are also useful in raising specific antibodies that can block the enzyme and effectively reduce its activity. Human serine/threonine protein kinase sequences can be used in the preparation of a medicament for modulating the activity of a serine/threonine protein kinase in a disease, e.g. cancer, diabetes, a central nervous system (CNS) disorder, a respiratory disorder (including chronic obstructive pulmonary disease), a cardiovascular disorder, a dermatological disorder, a gastrointestinal or liver disease, a haematological disorder, a musculoskeletal disorder, a reproductive disorder, or a urological disorder. CNS disorders may include Alzheimer's disease, Parkinson's disease, stroke or neuropathic pain

Sequence 1534 BP; 407 A; 362 C; 365 G; 400 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 9; Length 1534;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAGCTACTACTACA 381
|||||
894 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAGCTACTACTACA 953
|||||

382 ATCCAG 387

954 ATCCAG 959

RESULT 15

ACCT79967

ID ACC79967 standard; cDNA; 1534 BP.

ACCT79967;

09-SEP-2003 (first entry)

Human serine/threonine protein kinase encoding cDNA SEQ ID NO:1.

Human; serine/threonine protein kinase; kinase; enzyme; cytostatic; antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic; cerebroprotective; antiinflammatory; gastrointestinal; hepatotropic; gynaecological; uropathic; dermatological; gene therapy; cancer; diabetes; central nervous system disorder; CNS disorder; liver disease; respiratory disorder; chronic obstructive pulmonary disease; stroke; cardiovascular disorder; dermatological disorder; urological disorder; gastrointestinal disease; haematological disorder; Alzheimer's disease; musculoskeletal disorder; reproductive disorder; Parkinson's disease; neuropathic pain; gene; ss.

Homo sapiens.

Key Location/Qualifiers

104..1258

/*tag= a

/product= "serine/threonine protein kinase"

WO2003046167-A1.

```

XX 05-JUN-2003.
PD
XX
XX
PF 26-NOV-2002; 2002WO-EP013268.
XX
XX
PR 27-NOV-2001; 2001US-0333131P.
XX
XX
PA (FARB ) BAYER AG.
XX
XX
PI Koehler RH;
XX
XX
DR WPI; 2003-505196/47.
DR P-PSDB; ABR57357.
XX
XX
PT New polynucleotide encoding a serine/threonine protein kinase
PT polypeptide, useful for diagnosing, preventing or treating diseases
PT associated with serine/threonine protein kinase dysfunction, e.g. cancer
PT or diabetes.
XX
XX
PS Claim 1; Page 171-173; 196pp; English.
XX
XX
CC The present sequence encodes a human serine/threonine protein kinase (I).
CC (I) has cytosolic, antidiabetic, neuroprotective, antiparkinsonian,
CC nootropic, cerebrotective, analgesic, antiinflammatory, hepatotropic,
CC gastrointestinal, gynaecological, uropathic and dermatological
CC activities, and can be used in gene therapy. Serine/threonine protein
CC kinase polynucleotide and polypeptide sequences can be used in
CC diagnosing, preventing, ameliorating or treating diseases associated with
CC serine/threonine protein kinase dysfunction. They may also be used to
CC identify test compounds that may act, for example, as activators or
CC inhibitors at the enzyme's active site. The human serine/threonine
CC protein kinase and its fragments are also useful in raising specific
CC antibodies that can block the enzyme and effectively reduce its activity.
CC Human serine/threonine protein kinase sequences can be used in the
CC preparation of a medicament for modulating the activity of a serine/
CC threonine protein kinase in a disease, e.g. cancer, diabetes, a central
CC nervous system (CNS) disorder, a respiratory disorder (including chronic
CC obstructive pulmonary disease), a cardiovascular disorder, a
CC dermatological disorder, a gastrointestinal or liver disease, a
CC haematological disorder, a musculoskeletal disorder, a reproductive
CC disorder, or a urological disorder. CNS disorders may include Alzheimer's
CC disease, Parkinson's disease, stroke or neuropathic pain
XX
SQ Sequence 1534 BP; 407 A; 362 C; 365 G; 400 T; 0 U; 0 Other;
Query Match 16.1%; Score 66; DB 9; Length 1534;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 322 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAGCTACCTACTACA 381
Db 894 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAGCTACCTACTACA 953
QY 382 ATCCAG 387
Db 954 ATCCAG 959

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Search completed: January 13, 2005, 02:13:23
Job time : 408 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2005, 01:58:49 ; Search time 2946 Seconds
(without alignments)
5071.382 Million cell updates/sec

Title: US-10-786-065-3_COPY_50000_50409
Perfect score: 410
Sequence: 1 aatcatgataatcatgcag.....attatgattcagcttctga 410

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75.8	18.5	804	9	CR251670 Reverse s
2	66	16.1	481	1	AA436054 zu01c12.r
3	66	16.1	499	5	BX283916 BX283916
4	66	16.1	660	4	BX326162 BX326162
5	63.4	15.5	805	9	CEI37859 tigr-gse-
6	62	15.1	602	6	CD636748 56014973J
7	60.4	14.7	598	6	CD636752 56015001J
8	60.4	14.7	600	6	CD636753 56015009H
9	58.8	14.3	600	6	CD636739 56014901H
10	58.8	14.3	602	6	CD636757 56015025H
11	58	14.1	444	2	BB640105 BB640105
12	58	14.1	502	2	BB249604 BB249604
13	52.4	12.8	586	6	CD636749 56014981H
14	52.4	12.8	601	6	CD636760 56015089J
15	51	12.4	594	9	CE640507 tigr-gse-
16	48.4	11.8	600	6	CD636754 56015009J
17	48	11.7	600	6	CD636741 56014909H
18	46.4	11.3	314	6	CD636743 56014917H
19	46	11.2	602	6	CD636759 56015089H
20	45.8	11.2	601	6	CD636746 56014925J
21	45	11.0	599	6	CD636747 56014973H
22	44.4	10.8	602	6	CD636751 56015001H
23	44.4	10.8	602	6	CD636755 56015017H
24	43	10.5	1494	9	AG332059 Mus muscu

C 25	42.8	10.4	596	6	CD636758
C 26	42.8	10.4	603	6	CD636742
C 27	42.6	10.4	756	9	CNS06PD3
C 28	42.6	10.4	997	9	CNS005TE
C 29	42.2	10.3	868	9	AG499155 Mus muscu
C 30	42.2	10.3	1042	9	AG385616 Mus muscu
C 31	42.2	10.3	1065	9	AG289256 Mus muscu
C 32	42	10.2	1358	9	AG320427
C 33	41.4	10.1	1023	9	CL093094
C 34	41.2	10.0	812	8	B21426
C 35	41	10.0	628	5	BQ592805
C 36	40.6	9.9	774	8	B19116
C 37	40.2	9.8	890	9	CNS02AC6
C 38	40	9.8	1018	5	BQ899340
C 39	39.8	9.7	401	8	AQ784003
C 40	39.6	9.7	792	4	BG565997
C 41	39.4	9.6	758	9	AG276386
C 42	39.4	9.6	1154	9	CL082790
C 43	39.2	9.6	625	8	AZ464164
C 44	39.2	9.6	730	2	BF525539
C 45	39.2	9.6	913	9	CL465943

ALIGNMENTS

RESULT 1	CR251670	804 bp	DNA	linear	GSS 06-JUL-2004
LOCUS	Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN33n19, genomic survey sequence.				
DEFINITION	CR251670.1				
ACCESSION	CR251670.1				
VERSION	GSS; genome survey sequence; MICEP.				
KEYWORDS	GSS; genome survey sequence; MICEP.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 804)				
AUTHORS	Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICEP				
FEATURES	Location/Qualifiers				
source	1..804				
	/organism="Mus musculus"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:10090"				
	/clone_lib="MHPN"				

ORIGIN					
Query Match	18.5%;	Score 75.8;	DB 9;	Length 804;	
Best Local Similarity	83.5%;	Pred. NO. 4.7e-11;			
Matches	86;	Conservative	0;	Mismatches	17;
				Indels	0;
				Gaps	0;
Qy	293	CTCTCTTTTCTTTGTTGGCTTTATAGTCTGGAGTCCCTACAGGATACCTG	352		
Db	412	CTTACCTTTCTTTCTCTGCTCTGTAGGTTCTGGAGTCCCTACAGGATACCTG	471		
Qy	353	GCCGGAGTCTCCCAAGCTACCTAACTCAATCCAGGTAATATT	395		
Db	472	GCTTGGAGTCTCCCAACTGCTTAATCCAGGTAATATT	514		

RESULT 2	AA436054	481 bp	mRNA	linear	EST 09-NOV-1997
LOCUS	zu01c12.r1 Soares testis NHT Homo sapiens cdna clone IMAGE:730582				
DEFINITION	5' similar to gb:X66363 SERINE/THREONINE-PROTEIN KINASE PCTAIRB-1 (HUMAN); mRNA sequence.				

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AA436054 AA436054.1 EST. Homo sapiens (human)	1 GI:2140968	REFERENCE AUTHORS TITLE JOURNAL COMMENT	1 (bases 1 to 499) Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B. Human Unigeneset - RZPD3 Unpublished (2003) Contact: Ina Rofls RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGP9580141276. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi- bin/showLib.pl.cgi/?response?libNo=972 Contact: Ina Rofls RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: pCMV-M13u, Primer sequence: CGTTGTAAACGACGCCAGT.
FEATURES source	1..499 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGP9580141276 ; IMAGE:4563301" /tissue_type="renal cell adenocarcinoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC_14" /notes="Organ: Kidney; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."			
ORIGIN	Query Match 16.1%; Score 66; DB 5; Length 499; Best Local Similarity 100.0%; Pred. No. 3.1e-08; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 322 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCGGGAGTCTCCAGCTACCTACTACA 381 DB 113 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCGGGAGTCTCCAGCTACCTACTACA 172 QY 382 ATCCAG 387 DB 173 ATCCAG 178			
RESULT 4 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	BG326162 602425156F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4563301 5', mRNA sequence. BG326162 BG326162.1 GI:13132599 EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 660) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory			
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BX283916 BX283916 EST. Homo sapiens (human)	1 GI:28848370	REFERENCE AUTHORS TITLE JOURNAL COMMENT	1 (bases 1 to 481) Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenger, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 702 Std Error: 0.00 Seq primer: -28mi3 rev2 ET from Amersham High quality sequence stop: 442. Location/Qualifiers 1..481 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:5927210" /db_xref="taxon:9606" /clone="IMAGE:730582" /sex="male" /lab_host="DH10B" /clone_lib="Soares testis NHT" /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5'] TGTTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTTTTTT 3'. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN	Query Match 16.1%; Score 66; DB 1; Length 481; Best Local Similarity 100.0%; Pred. No. 3.1e-08; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 322 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCGGGAGTCTCCAGCTACCTACTACA 381 DB 225 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCGGGAGTCTCCAGCTACCTACTACA 284 QY 382 ATCCAG 387 DB 285 ATCCAG 290			
RESULT 3 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BX283916 BX283916 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4563301 EST. Homo sapiens (human)	1 GI:28848370	REFERENCE AUTHORS TITLE JOURNAL COMMENT	1 (bases 1 to 499 bp mRNA linear EST 05-MAR-2003 IMAGE:4563301, mRNA sequence. BX283916 BX283916.1 GI:28848370 EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC1276 row: 0 column: 14
High quality sequence stop: 658.
Location/Qualifiers
1. .660

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4563301"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 14"
/note="Organ: Kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 16.1%; Score 66; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAGCTACCTACTACA 381
|||||
DB 111 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAGCTACCTACTACA 170
|||||
QY 382 ATCCAG 387
|||||
DB 171 ATCCAG 176

RESULT 5
CE137859
LOCUS tigr-gss-dog-17000371210778 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE137859
CE137859.1 GI:35244514
GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 805)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.
Location/Qualifiers
1. .805
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4563301"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 14"
/note="Organ: Kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 15.5%; Score 63.4; DB 9; Length 805;
Best Local Similarity 67.7%; Pred. No. 2.1e-07;
Matches 105; Conservative 0; Mismatches 46; Indels 4; Gaps 1;

QY 102 CCCCGACCATAGGAATGTATTACAGTTTTGCCCAAGAAACACAAACGTTGGAAACACT 161
|||||
DB 642 CACAGGATTTAAGAATACATAACAGTTTGGCCCATGAAACTACAAATATGGGTGACACT 701
|||||
QY 162 CAAATTTCTTCTCGTATACATCAGCTGGTGTGCATGCAATGGGACATACCATCTGACGCT 221
|||||
DB 702 AAGATTTCTTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 757
|||||
QY 222 TCCCTGTCTTCCCGGATTTGCTCGCATGCTCTCC 256
|||||
DB 758 TCCCTATTCTCCCTGATCTGTTCTTCATGCTCTCC 792
|||||

RESULT 6
CD636748/c
LOCUS CD636748 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004
DEFINITION S6014973J1
ACCESSION CD636748
VERSION CD636748.1 GI:40285015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 602)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Fu G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. .602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

FEATURES
source
Location/Qualifiers
1. .602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 15.1%; Score 62; DB 6; Length 602;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAGCTACCTACTACA 381
|||||
DB 62 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAGCTACCTACTACA 3
|||||
QY 382 AT 383
|||||
DB 2 AT 1

RESULT 7
CD636752/c
LOCUS CD636752 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004
DEFINITION S6015001J1
ACCESSION CD636752
VERSION CD636752.1 GI:40285019
KEYWORDS EST.
SOURCE Homo sapiens (human)


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/db_xref="taxon:9606"
/clone_lib="FLP"
/notes="Vector: pDrive Cloning Vector"

ORIGIN
Query Match      14.3%; Score 58.8; DB 6; Length 602;
Best Local Similarity 96.8%; Pred. No. 4.4e-06;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 322 AGGTCCTGGAGTCCCTACAGAGGATACCTTGCCGGGAGTCTCCAACTACCTACTACA 381
    |||||||
Db 540 AGGTCCTGGAGTCCCTACAGAGGATACCTTGCCGGGAGTCTCCAACTACCTACTACA 599
    |||||||

Qy 382 AT 383
    ||
Db 600 AT 601

RESULT 11
BB640105      444 bp      mRNA      linear      EST 31-AUG-2001
DEFINITION   BB640105 RIKEN full-length enriched, 7 days neonate cerebellum Mus
              musculus cDNA clone A730034C03 5', mRNA sequence.
ACCESSION    BB640105
VERSION      BB640105.1 GI:15401501
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 444)
              Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
              Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
              Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
              Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
              Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
              Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
              Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
              RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
              Unpublished (2001)
              Contact: Yoshihide Hayashizaki
              Laboratory for Genome Exploration Research Group, RIKEN Genomic
              Sciences Center(GSC), Yokohama Institute
              The Institute of Physical and Chemical Research (RIKEN)
              1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
              Tel: 81-45-503-9222
              Fax: 81-45-503-9216
              Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
              Carninci,P., Shibata,K., Hayatsu,N., Sugahara,Y., Shibata,K.,
              Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
              Normalization and subtraction of cap-trapper-selected cDNAs to
              prepare full-length cDNA libraries for rapid discovery of new
              genes. Genome Res. 10 (10), 1617-1630 (2000)
              wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
              Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
              Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
              and Hayashizaki,Y.
              RIKEN integrated sequence analysis (RISA) system--384-format
              sequencing pipeline with 384 multicapillary sequencer. Genome Res.
              10 (11), 1757-1771 (2000)
              Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
              Sugahara,Y. and Hayashizaki,Y.
              Computer-based methods for the mouse full-length cDNA
              encyclopedia: real-time sequence clustering for construction of a
              nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
              Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A.,
              Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
              Arakawa,T., Ishii,Y. and Hayashizaki,Y.
              Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
              Func. Genomics 2 pre, 172-186 (2001)
              Please visit our web site (http://genome.gsc.riken.go.jp) for
              further details.
              e mouse tissues.

ORIGIN
Query Match      14.1%; Score 58; DB 2; Length 444;
Best Local Similarity 92.4%; Pred. No. 6.9e-06;
Matches 61; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 322 AGGTCCTGGAGTCCCTACAGAGGATACCTTGCCGGGAGTCTCCAACTACCTACTACA 381
    |||||||
Db 213 AGGTCCTGGAGTCCCTACAGAGGATACCTTGCCGGGAGTCTCCAACTACCTACTACA 272
    |||||||

Qy 382 ATCCAG 387
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Db 273 ATCCAG 278

RESULT 12
BB249604
LOCUS        BB249604
DEFINITION   BB249604 RIKEN full-length enriched, 7 days neonate cerebellum Mus
              musculus cDNA clone A730034C03 3', mRNA sequence.
ACCESSION    BB249604
VERSION      BB249604.2 GI:15410630
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 502)
              Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
              Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
              Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
              Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
              Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
              Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
              Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
              RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
              Unpublished (2001)
              On Jul 6, 2000 this sequence version replaced gi:8942350.
              Contact: Yoshihide Hayashizaki
              Laboratory for Genome Exploration Research Group, RIKEN Genomic
              Sciences Center(GSC), Yokohama Institute
              The Institute of Physical and Chemical Research (RIKEN)
              1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
              Tel: 81-45-503-9222
              Fax: 81-45-503-9216

```

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 waki, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Kira, A.,
 Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.,
 and Hayashizaki, Y. sequence analysis (RISA) system--384-format
 RIKEN integrated sequence analysis with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A.,
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K.,
 Arakawa, T., Ishii, Y. and Hayashizaki, Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
 Funct. Genomics 2 pre, L72-L86 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for
 further details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Location/Qualifiers
 source
 1..502
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A730034C03"
 /tissue types="cerebellum"
 /dev stages="7 days neonate"
 /lab_host="DH10B"
 /clone_libs="RIKEN full-length enriched, 7 days neonate
 cerebellum"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGGAGGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 20.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGGAGGATTCGAGTTAATTAATTAATTCCTCCCTCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from lambda
 FLC I."

ORIGIN
 source
 Query Match 14.1%; Score 58; DB 2; Length 502;
 Best Local Similarity 92.4%; Pred. No. 7.2e-06;
 Matches 61; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 322 AGGTCCTGGAGTCCCTACAGGATCTTGGCGGGAGTCTCCAGCTACTACTACA 381
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 Db
 QY 382 ATCCAG 387
 199 ATCCAG 204

RESULT 13
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 LOCUS 56014981H1 FLP Homo sapiens cDNA, mRNA sequence.
 DEFINITION CD636749
 ACCESSION CD636749
 VERSION CD636749.1 GI:40285016
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 Genomics 84 (1), 205-210 (2004)
 CONTACT: Fu GK
 INCYTE Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.
 Location/Qualifiers
 source
 1..586
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_libs="FLP"
 /note="Vector: pDrive Cloning Vector"
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 Query Match 12.8%; Score 52.4; DB 6; Length 586;
 Best Local Similarity 98.1%; Pred. No. 0.00034;
 Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 322 AGGTCTGGAGTCCCTACAGGATCTTGGCGGGAGTCTCCAGCTACTACTA 375
 525 AGGTCTGGAGTCCCTACAGGATCTTGGCGGGAGTCTCCAGCTACTACTA 578
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 RESULT 14
 CD636760 601 bp mRNA linear EST 12-JAN-2004
 LOCUS 56015089J1 FLP Homo sapiens cDNA, mRNA sequence.
 DEFINITION CD636760
 ACCESSION CD636760
 VERSION CD636760.1 GI:40285027
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 Genomics 84 (1), 205-210 (2004)
 CONTACT: Fu GK
 INCYTE Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.
 Location/Qualifiers
 source
 1..601
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_libs="FLP"
 /note="Vector: pDrive Cloning Vector"
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 Query Match 12.8%; Score 52.4; DB 6; Length 601;
 Best Local Similarity 98.1%; Pred. No. 0.00034;
 Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 AGGTGCTGGAGTCCCTACAGAGGATACCTGGCCGGAGTCTCCAAGCTACCTA 375
 Db |||||
 540 AGGTGCTGGAGTCCCTACAGAGGATACCTGGCCGGAGTCTCCAAGCTACCAA 593

RESULT 15
 CE640507
 LOCUS tigr-gss-dog-17000366827968 594 bp DNA linear GSS 29-SEP-2003
 DEFINITION genomic survey sequence.
 ACCESSION CE640507
 VERSION CE640507.1 GI:36958177
 KEYWORDS GSS:
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 594)
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
 Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627

COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun..

FEATURES
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 Location/Qualifiers
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 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
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 Best Local Similarity 80.0%; Pred. No. 0.00088;
 Matches 60; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 66 TCTGCCTCAGACAA 80
 Db |||||

Search completed: January 13, 2005, 03:35:05
 Job time : 2949 secs

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2005, 02:05:04 ; Search time 87 Seconds
(without alignments)
3349.695 Million cell updates/sec

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Perfect score: 410

Sequence: 1 aatcgtatgataatcatgcag.....atatgatctgagcttctga 410

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	410	100.0	53332	4	US-09-801-861-3
2	410	100.0	53332	4	US-10-224-562-3
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4	87.4	21.3	2203	4	US-10-224-562-1
5	66	16.1	481	3	US-09-387-212-14
6	66	16.1	481	4	US-09-948-802-14
7	66	16.1	1308	4	US-09-801-861-4
8	66	16.1	1308	4	US-10-224-562-4
9	48.2	11.8	7218	1	US-08-232-463-14
10	34.6	8.4	6405	3	US-09-281-481A-18
11	34.2	8.3	1087	3	US-08-991-789A-4
12	34.2	8.3	1087	3	US-09-062-451-4
13	34.2	8.3	1087	4	US-09-598-326-4
14	34.2	8.3	1087	4	US-09-289-198-4
15	34.2	8.3	1087	4	US-09-429-755-4
16	33.8	8.2	257	4	US-09-513-999C-34168
17	33.8	8.2	3271	3	US-08-545-196B-22
18	33.2	8.1	5152	4	US-10-204-708-48
19	33	8.0	308	4	US-09-513-999C-16871
20	32.8	8.0	31728	3	US-09-453-702B-64
21	32.6	8.0	399	4	US-09-621-976-8976
22	32.2	7.9	1044	4	US-08-956-171E-648
23	32.2	7.9	1044	4	US-08-781-986A-648
24	32	7.8	155	4	US-09-513-999C-25805
25	32	7.8	73395	4	US-09-984-890-3
26	32	7.8	73395	4	US-10-274-194-3
27	31.4	7.7	1884	4	US-09-248-796A-6511

c 28	31.4	7.7	786431	4	US-09-751-389-3	Sequence 3, Appli
c 29	31.2	7.6	273	4	US-09-313-294A-897	Sequence 897, App
c 30	31.2	7.6	292	4	US-09-313-294A-4357	Sequence 4357, Ap
c 31	31.2	7.6	451	4	US-09-513-999C-32372	Sequence 32372, A
c 32	31.2	7.6	1161	4	US-09-023-655-1373	Sequence 1373, Ap
c 33	31.2	7.6	1825	4	US-09-620-312D-313	Sequence 313, App
c 34	31.2	7.6	99500	3	US-09-798-096-10	Sequence 10, Appl
c 35	30.8	7.5	834	4	US-09-621-976-2574	Sequence 2574, Ap
c 36	30.8	7.5	53526	3	US-08-658-136-2	Sequence 2, Appli
c 37	30.8	7.5	53577	3	US-08-658-136-1	Sequence 1, Appli
c 38	30.6	7.5	248	3	US-09-007-005-32	Sequence 32, Appl
c 39	30.6	7.5	248	3	US-09-244-796-32	Sequence 32, Appl
c 40	30.6	7.5	277	3	US-09-007-005-3	Sequence 3, Appli
c 41	30.6	7.5	277	3	US-09-244-796-3	Sequence 3, Appli
c 42	30.6	7.5	338	2	US-08-454-557C-97	Sequence 97, Appl
c 43	30.6	7.5	338	2	US-08-340-426D-97	Sequence 97, Appl
c 44	30.6	7.5	338	2	US-08-450-673C-97	Sequence 97, Appl
c 45	30.6	7.5	338	5	PCT-US95-17111A-97	Sequence 97, Appl

ALIGNMENTS

RESULT 1

US-09-801-861-3

; Sequence 3, Application US/09801861

; Patent No. 6492154

; GENERAL INFORMATION:

; APPLICANT: YAN, Chunhua et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE OF INVENTION: THEREOF

; FILE REFERENCE: CL01098

; CURRENT APPLICATION NUMBER: US/09/801.861

; CURRENT FILING DATE: 2001-03-09

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 53332

; TYPE: DNA

; ORGANISM: Human

US-09-801-861-3

Query Match 100.0%; Score 410; DB 4; Length 53332;
Best Local Similarity 100.0%; Pred. No. 8.2e-128;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TATGATCTGCTCAGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	120
Db	50060	TATGATCTGCTCAGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	50119
Qy	121	ATTACAGTTTTCGCCAAGAAACCAACAGTTTGGAAACACTCAAGTTTCTTCTCGTATA	180
Db	50120	ATTACAGTTTTCGCCAAGAAACCAACAGTTTGGAAACACTCAAGTTTCTTCTCGTATA	50179
Qy	181	CATCAGCTGGTGTATGCAATGGGACATACATCTGAGCTTCCCTGTCTTCCCTGATT	240
Db	50180	CATCAGCTGGTGTATGCAATGGGACATACATCTGAGCTTCCCTGTCTTCCCTGATT	50239
Qy	241	TGTCCTCATGCTCCCAATACCTCTTTTCCCAACCACTCATCTCCCACTCCCTTCTTCTT	300
Db	50240	TGTCCTCATGCTCCCAATACCTCTTTTCCCAACCACTCATCTCCCACTCCCTTCTTCTT	50299
Qy	301	TTTCTTTTGGCTTTTATATAGTGTGGGAGTCCCTTACAGAGATACCTTTGGCGGGAG	360
Db	50300	TTTCTTTTGGCTTTTATATAGTGTGGGAGTCCCTTACAGAGATACCTTTGGCGGGAG	50359
Qy	361	TCTCAAGTACCTAACTACAACTCAAGTAATATGATCTGAGCTTCTGA	410


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Db 225 AGGTCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 284
Qy 382 ATCCAG 387
Db 285 ATCCAG 290

RESULT 6
US-09-948-802-14
; Sequence 14, Application US/09948802
; Patent No. 6465232
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 2001-09-07
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-948-802-14

Query Match 16.1%; Score 66; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 2e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 66; Conservative 0;

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Qy 382 ATCCAG 387
Db 285 ATCCAG 290

RESULT 7
US-09-801-861-4
; Sequence 4, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Release 1.0, Version #1.25
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-4

Query Match 16.1%; Score 66; DB 4; Length 1308;
Best Local Similarity 100.0%; Pred. No. 3.3e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 66; Conservative 0;

Qy 322 AGGTCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 381
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Qy 382 ATCCAG 387
Db 1004 ATCCAG 1009

RESULT 8
US-10-224-562-4
; Sequence 4, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEROF
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-10-224-562-4

Query Match 16.1%; Score 66; DB 4; Length 1308;
Best Local Similarity 100.0%; Pred. No. 3.3e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 66; Conservative 0;

Qy 322 AGGTCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 381
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Qy 382 ATCCAG 387
Db 1004 ATCCAG 1009

RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOMLOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 INMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
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Thu Jan 13 09:56:04 2005

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; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

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Best Local Similarity 7.9%; Pred. No. 8.2e-06;
Matches 17; Conservative 125; Mismatches 73; Indels 0; Gaps 0;

QY 166 TTCTCTTCGTATACATCAGCTGGTGCATGCAATGCGGACATACCATCTGAGCGTTCC 225
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QY 226 TGTTCTCCCTGATTTGCTCGCATGCTCCAATACCTCTTTCCAACCACTCACTCC 285
Db 1309 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1368
QY 286 CACCTCACCTTCTTTCTTTGTTGGCTTTATATAGTGCTGGAGTCCCTACAGAG 345
Db 1369 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1428
QY 346 ATACTGGCGGGAGTCTCCAAGCTACCTAATAC 380
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RESULT 10
US-09-281-481A-18/c
; Sequence 18, Application US/09281481A
; Patent No. 6383747
; GENERAL INFORMATION:
; APPLICANT: DAMKINS, Roger L. and ABRAHAM, Lawrence J.
; TITLE OF INVENTION: GENETIC ANALYSIS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/281.481A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,971
; FILING DATE: 16-JUL-1997
; APPLICATION NUMBER: US 232,229
; FILING DATE: 29-APR-1994
; APPLICATION NUMBER: PK9279 (AU)
; FILING DATE: 01-NOV-1991
; APPLICATION NUMBER: PCT/AU92/00583
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, FRANK S
; REFERENCE/DOCKET NUMBER: 9279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: +516 742 4343
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 6405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-281-481A-18

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Best Local Similarity 51.6%; Pred. No. 0.31;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 186 GCTGTGTGCATGCAATGGGACATACCATCTGACCGCTTCCGCTTCTTCCCTGATTGTCC 245
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QY 246 TGCATGCTCCAAATACCTTTTCCAACCACTCATCTCCCACTCACCTTTCTTTTCT 305
Db 4790 TTGTTTGAATAATTAATCACTAGAACCCACCATACTGCGCGCTGACCACTTCTTCT 4731
QY 306 TTGTTTGGCTTTATATAGGTGCTGGAGTCCCT 338
Db 4730 TTTTCTCTCTCAATTTGTGTATGATTCTCT 4698
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RESULT 11
US-08-991-789A-4
; Sequence 4, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 292
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991.789A
; FILING DATE: 11-Dec-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-991-789A-4

Query Match 8.3%; Score 34.2; DB 3; Length 1087;
Best Local Similarity 53.3%; Pred. No. 0.17;
Matches 72; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 274 ACCTGATCTCCCACTCACCTTCTTTTCTTTGTTGGCTTTATATAGTGTGGAG 333
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Db 189 ACCTCAGGCTCCACCATACCCAGAGTGTCTGGTTTGTAAATTACTGCCAGGTT 248
Qy 334 TCCCTACAGAGATACCTTGGCCGGGAGTCTCCAGCTACCTTAACCTACCAATCCAGGTAATA 393
Db 249 TCAGCTCAGATATCCCTGGAGGAATATTCAGATTCCTCAGTAGTTTCCAGGTTAAA 308
Qy 394 TTGATCTGAGCTTCT 408
Db 309 ATCTATAGGCTTCT 323

RESULT 12
US-09-062-451-4
; Sequence 4, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,451
; FILING DATE: 04-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.419C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-062-451-4

Query Match 8.3%; Score 34.2; DB 3; Length 1087;
Best Local Similarity 53.3%; Pred. No. 0.17; Mismatches 63; Indels 0; Gaps 0;
Matches 72; Conservative 0

Qy 274 ACCTCATCTCCACCTCACCTTTCTTTTCTTTGGTCTTATATAGTGTGGGAG 333
Db 189 ACCTCAGGCTCCACCATACCCAGAGTGTCTGGTTTGTAAATTACTGCCAGGTT 248
Qy 334 TCCCTACAGAGATACCTTGGCCGGGAGTCTCCAGCTACCTTAACCTACCAATCCAGGTAATA 393
Db 249 TCAGCTCAGATATCCCTGGAGGAATATTCAGATTCCTCAGTAGTTTCCAGGTTAAA 308
Qy 394 TTGATCTGAGCTTCT 408
Db 309 ATCTATAGGCTTCT 323

RESULT 13
US-09-598-326-4
; Sequence 4, Application US/09598326

; Patent No. 6423496
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 247
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,326
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-598-326-4

Query Match 8.3%; Score 34.2; DB 4; Length 1087;
Best Local Similarity 53.3%; Pred. No. 0.17; Mismatches 63; Indels 0; Gaps 0;
Matches 72; Conservative 0

Qy 274 ACCTCATCTCCACCTCACCTTTCTTTTCTTTGGTCTTATATAGTGTGGGAG 333
Db 189 ACCTCAGGCTCCACCATACCCAGAGTGTCTGGTTTGTAAATTACTGCCAGGTT 248
Qy 334 TCCCTACAGAGATACCTTGGCCGGGAGTCTCCAGCTACCTTAACCTACCAATCCAGGTAATA 393
Db 249 TCAGCTCAGATATCCCTGGAGGAATATTCAGATTCCTCAGTAGTTTCCAGGTTAAA 308
Qy 394 TTGATCTGAGCTTCT 408
Db 309 ATCTATAGGCTTCT 323

RESULT 14
US-09-289-198-4
; Sequence 4, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C5
; CURRENT APPLICATION NUMBER: US/09/289,198
; CURRENT FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: US 09/062,451
; EARLIER FILING DATE: 1998-04-17

Thu Jan 13 09:56:04 2005

EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1087
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1087)
OTHER INFORMATION: n = A,T,C or G

US-09-289-198-4

Query Match 8.3%; Score 34.2; DB 4; Length 1087;
Best Local Similarity 53.3%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 72; Conservative 0; Mismatches 63;
QY 274 ACTCATCTCCACCTCACCCTTTCTTTTCTTTGGCTTATATAGGTGCTGGGAG 333
DB 189 ACCTCAGGCTCCAACTACCCCAAGAGTTGTTGTTTAAATTAATCTCCAGGTTAA 248
QY 334 TCCCTACAGAGGATCTTGGCCGGAGTCTCCAACTACCTAACTACCAATCCAGGTAATA 393
DB 249 TCAGCTGCAGATATCCCTCGAAGGAATATTCAGATTCCCTGAGTAGTTCCAGGTTAAA 308
QY 394 TTGATCTGAGCTTCT 408
DB 309 ATCCTATAGGCTTCT 323

RESULT 15

US-09-429-755-4
Sequence 4, Application US/09429755A
Patent No. 6656480
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Mishner, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1087
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1087)
OTHER INFORMATION: n = A,T,C or G

US-09-429-755-4

Query Match 8.3%; Score 34.2; DB 4; Length 1087;
Best Local Similarity 53.3%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 72; Conservative 0; Mismatches 63;
QY 274 ACTCATCTCCACCTCACCCTTTCTTTTCTTTGGCTTATATAGGTGCTGGGAG 333

Db 189 ACCTCAGGCTCCAACTACCCCAAGAGTTGTTGTTTAAATTAATCTCCAGGTT 248
QY 334 TCCCTACAGAGGATCTTGGCCGGAGTCTCCAACTACCTAACTACCAATCCAGGTAATA 393
DB 249 TCAGCTGCAGATATCCCTCGAAGGAATATTCAGATTCCCTGAGTAGTTCCAGGTTAAA 308
QY 394 TTGATCTGAGCTTCT 408
DB 309 ATCCTATAGGCTTCT 323

Search completed: January 13, 2005, 03:36:42
Job time : 89 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	410	100.0	53332	9	US-09-801-861-3	Sequence 3, Appli
2	410	100.0	53332	14	US-10-224-562-3	Sequence 3, Appli
3	87.4	21.3	2203	9	US-09-801-861-1	Sequence 1, Appli
4	87.4	21.3	2203	14	US-10-224-562-1	Sequence 1, Appli
5	66	16.1	481	9	US-09-948-802-14	Sequence 14, Appl
6	66	16.1	481	15	US-10-121-925-14	Sequence 14, Appl
7	66	16.1	1308	9	US-09-801-861-4	Sequence 4, Appli
8	66	16.1	1308	14	US-10-224-562-4	Sequence 4, Appli
9	66	16.1	1376	16	US-10-466-759-15	Sequence 15, Appl
10	66	16.1	2250	18	US-10-618-941-20	Sequence 20, Appl
11	66	16.1	3210	16	US-10-425-114-26244	Sequence 26244, A
12	66	9.3	113515	15	US-10-311-455-2148	Sequence 2148, Ap
C	38.2	19.3	113515	15	US-10-311-455-2148	Sequence 2148, Ap

; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-948-802-14

Query Match 16.1%; Score 66; DB 9; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 225 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 284

QY 382 ATCCAG 387
DB 285 ATCCAG 290

RESULT 6

US-10-121-925-14
; Sequence 14, Application US/10121925
; Publication No. US20030104505A1
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/10/121,925
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/948,802
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-121-925-14

Query Match 16.1%; Score 66; DB 15; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 225 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 284

QY 382 ATCCAG 387
DB 285 ATCCAG 290

RESULT 7

US-09-801-861-4
; Sequence 4, Application US/09801861
; Patent No. US20020119544A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-4

Query Match 16.1%; Score 66; DB 9; Length 1308;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 944 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 1003

QY 382 ATCCAG 387
DB 1004 ATCCAG 1009

RESULT 8

US-10-224-562-4
; Sequence 4, Application US/10224562
; Publication No. US20030022229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-10-224-562-4

Query Match 16.1%; Score 66; DB 14; Length 1308;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 944 AGGTCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 1003

QY 382 ATCCAG 387
DB 1004 ATCCAG 1009

RESULT 9

US-10-466-759-15
; Sequence 15, Application US/10466759
; Publication No. US20040081983A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: LEE, Ernestine A.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: ISON, Craig H.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: JACKSON, Jennifer L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: TRAN, Bao
; APPLICANT: DING, Li
; APPLICANT: LU, Dying Aina M.

Thu Jan 13 09:56:04 2005

APPLICANT: LAL, Preeti G.
APPLICANT: WARREN, Bridget A.
TITLE OF INVENTION: KINASES AND PHOSPHATASES
FILE REFERENCE: PI-0344 USN
CURRENT APPLICATION NUMBER: US/10/466,759
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: PCT/US02/01369
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/263,083
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/271,205
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/271,117
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/276,859
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/278,504
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/278,522
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/280,510
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/280,266
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL Program
SEQ ID NO 15
LENGTH: 1376
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7494145CB1
US-10-466-759-15

Query Match 16.1%; Score 66; DB 16; Length 1376;
Best Local Similarity 100.0%; Pred. No. 2.7e-11; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 0;

QY 322 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 1088 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 1147

QY 382 ATCCAG 387
DB 1148 ATCCAG 1153

RESULT 10
US-10-618-941-20
Sequence 20, Application US/10618941
Publication No. US20040197792A1
GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patent version 3.2
SEQ ID NO 20
LENGTH: 2250
TYPE: DNA
ORGANISM: Homo sapiens
US-10-618-941-20

Query Match 16.1%; Score 66; DB 18; Length 2250;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 988 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 1047

QY 382 ATCCAG 387
DB 1048 ATCCAG 1053

RESULT 11
US-10-425-114-26244
Sequence 26244, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26244
LENGTH: 3210
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4119-079-Cl_FLI
US-10-425-114-26244

Query Match 16.1%; Score 66; DB 16; Length 3210;
Best Local Similarity 100.0%; Pred. No. 4.1e-11; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 0;

QY 322 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 560 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 619

QY 382 ATCCAG 387
DB 620 ATCCAG 625

RESULT 12
US-10-311-455-2148/c
Sequence 2148, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2148
LENGTH: 113515
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2148

Query Match          9.3%; Score 38.2; DB 15; Length 113515;
Best Local Similarity 55.7%; Pred. No. 0.67;
Matches 73; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 191 TGTGATGCAATGGGACATACCATCGAGCTTCCTGTTCTTCCTGATTTCTCTGCAT 250
Db 61960 TTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 61901

Qy 251 GTCCTCAATACCTCTTTTCAACACCTCATCTCCCACTCACCTTTCTTTCTTTCTTTGTT 310
Db 61900 TCCCTTCCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 61841

Qy 311 TGGCTTTTATAT 321
Db 61840 TCTCTTTCTCT 61830

RESULT 13
US-10-021-323-798/c
; Sequence 798, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 798
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-013-Q1-N6-A6
US-10-021-323-798

Query Match          9.0%; Score 37; DB 17; Length 543;
Best Local Similarity 60.4%; Pred. No. 0.13;
Matches 61; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 221 TTCCCTGTTCTTCCTGATTTGTCCTGCATGTCCTCAATACCTCTTTTCCAAACCACTCAT 280
Db 422 TTCCCTCTTTTGCCCATTTCTCTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 363

Qy 281 CTCCCACTCACCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTAT 321
Db 362 CCCCCTTTCTCCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTT 322

RESULT 14
US-09-796-692-3640/c
; Sequence 3640, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
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; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3640
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-3640

Query Match          8.9%; Score 36.4; DB 9; Length 285;
Best Local Similarity 58.2%; Pred. No. 0.15;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 221 TTCCCTGTTCTTCCTGATTTGTCCTGCATGTCCTCAATACCTCTTTTCCAAACCACTCAT 280
Db 110 TTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 51

Qy 281 CTCCCACTCACCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTAT 330
Db 50 CTCCCTGCCCCAACATCTCTGTGCCATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGG 1

RESULT 15
US-10-040-862-3640/c
; Sequence 3640, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
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us-10-786-065-3_copy_50000_50409.rnpb

Thu Jan 13 09:56:04 2005

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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3640
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-3640

Query Match      8.9%; Score 36.4; DB 14; Length 285;
Best Local Similarity 58.2%; Pred. No. 0.15; 46; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 46;

Qy 221 TTCCCTGTTCTCCCTGATTTCCTGCATGTCCTCAATACCTCTTTCCACCACTCAT 280
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Db 110 TTCCCTGTTCTCCCTGATTTCCTGCATGTCCTCAATACCTCTTTCCACCACTCAT 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 281 CTCCTGCTCCCAACATCCTGTGCTCATCCCTGTGCTTATATAGGTGCTGG 330
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 50 CTCCTGCTCCCAACATCCTGTGCTCATCCCTGTGCTTATATAGGTGCTGG 1
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Search completed: January 13, 2005, 07:01:54
Job time : 4988 secs